



1600

RAW SEQUENCE LISTING

DATE: 09/25/2003

PATENT APPLICATION: US/09/579,949

TIME: 13:19:30

Input Set : A:\03848-00006.ST25.txt

Output Set: N:\CRF4\09252003\I579949.raw

3 <110> APPLICANT: Winkler, James
 4 Fodor, Stephen
 5 Buchko, Christopher
 6 Ross, Debra
 7 Aldwin, Lois
 8 Modlin, Douglas
 10 <120> TITLE OF INVENTION: COMBINATORIAL STRATEGIES FOR POLYMER SYNTHESIS
 12 <130> FILE REFERENCE: 03848-00006
 14 <140> CURRENT APPLICATION NUMBER: 09/579,949
 C--> 15 <141> CURRENT FILING DATE: 2003-05-26
 17 <150> PRIOR APPLICATION NUMBER: 09/498,554
 18 <151> PRIOR FILING DATE: 2000-02-04
 20 <150> PRIOR APPLICATION NUMBER: 09/129,463
 21 <151> PRIOR FILING DATE: 1998-08-04
 23 <150> PRIOR APPLICATION NUMBER: 08/426,202
 24 <151> PRIOR FILING DATE: 1995-04-21
 26 <150> PRIOR APPLICATION NUMBER: 07/980,523
 27 <151> PRIOR FILING DATE: 1992-11-20
 29 <150> PRIOR APPLICATION NUMBER: 07/874,849
 30 <151> PRIOR FILING DATE: 1992-04-24
 32 <150> PRIOR APPLICATION NUMBER: 07/796,243
 33 <151> PRIOR FILING DATE: 1991-11-22
 35 <160> NUMBER OF SEQ ID NOS: 6
 37 <170> SOFTWARE: PatentIn version 3.1
 39 <210> SEQ ID NO: 1
 40 <211> LENGTH: 5
 41 <212> TYPE: PRT
 42 <213> ORGANISM: Artificial Sequence
 44 <220> FEATURE:
 45 <223> OTHER INFORMATION: peptide
 47 <400> SEQUENCE: 1
 49 Tyr Gly Gly Phe Leu
 50 1 5
 53 <210> SEQ ID NO: 2
 54 <211> LENGTH: 5
 55 <212> TYPE: PRT
 56 <213> ORGANISM: Artificial Sequence
 58 <220> FEATURE:
 59 <223> OTHER INFORMATION: peptide
 61 <220> FEATURE:
 62 <221> NAME/KEY: MISC_FEATURE
 63 <222> LOCATION: (2)..(2)
 64 <223> OTHER INFORMATION: Xaa is a D amino acid

**Does Not Comply
Corrected Diskette Need d**

*Insufficient explanation
give source of genetic material
see item 11 on error summary
sheet.*

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```

67 <400> SEQUENCE: 2
W--> 69 Tyr Xaa Gly Phe Leu
70 1 5
73 <210> SEQ ID NO: 3
74 <211> LENGTH: 5
75 <212> TYPE: PRT
76 <213> ORGANISM: Artificial Sequence
78 <220> FEATURE:
79 <223> OTHER INFORMATION: peptide
81 <220> FEATURE:
82 <221> NAME/KEY: MISC_FEATURE
83 <222> LOCATION: (1)..(1)
84 <223> OTHER INFORMATION: Xaa is a D amino acid
87 <400> SEQUENCE: 3
W--> 89 Xaa Gly Gly Phe Leu
90 1 5
93 <210> SEQ ID NO: 4
94 <211> LENGTH: 8
95 <212> TYPE: DNA
96 <213> ORGANISM: Artificial Sequence
98 <220> FEATURE:
99 <223> OTHER INFORMATION: primer
101 <400> SEQUENCE: 4
102 gccgacgc 8
105 <210> SEQ ID NO: 5
106 <211> LENGTH: 8
107 <212> TYPE: DNA
108 <213> ORGANISM: Artificial Sequence
110 <220> FEATURE:
111 <223> OTHER INFORMATION: primer
113 <220> FEATURE:
114 <221> NAME/KEY: misc_feature
115 <222> LOCATION: (8)..(8)
116 <223> OTHER INFORMATION: a fluorescein molecule is coupled to the 3' end
119 <400> SEQUENCE: 5
120 gcgtcggc 8
123 <210> SEQ ID NO: 6
124 <211> LENGTH: 5
125 <212> TYPE: PRT
126 <213> ORGANISM: Artificial Sequence
128 <220> FEATURE:
129 <223> OTHER INFORMATION: peptide
131 <220> FEATURE:
132 <221> NAME/KEY: MISC_FEATURE
133 <222> LOCATION: (1)..(2)
134 <223> OTHER INFORMATION: Xaa is a D amino acid
137 <400> SEQUENCE: 6
W--> 139 Xaa Xaa Gly Phe Leu
140 1 5

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RAW SEQUENCE LISTING ERROR SUMMARY

DATE: 09/25/2003

PATENT APPLICATION: US/09/579,949

TIME: 13:19:31

Input Set : A:\03848-00006.ST25.txt

Output Set: N:\CRF4\09252003\I579949.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; Xaa Pos. 2

Seq#:3; Xaa Pos. 1

Seq#:6; Xaa Pos. 1,2

VERIFICATION SUMMARY

DATE: 09/25/2003

PATENT APPLICATION: US/09/579,949

TIME: 13:19:31

Input Set : A:\03848-00006.ST25.txt

Output Set: N:\CRF4\09252003\I579949.raw

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:69 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:89 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:139 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

09 | 579,949

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

 - 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

 - 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use **space characters**, instead.

 - 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

 - 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

 - 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

 - 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

 - 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

 - 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

 - 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

 - 11 X Use of <220> Sequence(s) 1-3, 6 missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

 - 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

 - 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid